

- (a) hybridizing a single strand DNA molecule with a complementary reference DNA strand to form a test duplex;
- (b) separating the test duplex from at least one control duplex run in the same separation;
- (c) detecting the positions to which the test duplex and the at least one control duplex migrate in the separation;
- (d) assigning an exact migration value to the position to which the test duplex migrates; and
- (e) identifying the DNA molecule by matching the exact migration value with a database of migration values of identified DNA molecules.

56.(New) The method of claim 55 wherein the complementary reference DNA strand is labeled.

57.(New) The method of claim 55 further comprising repeating steps (a)–(e) one or more times wherein a different complementary reference strand is utilized in each repeat of steps (a)–(e) to identify the DNA molecule.

58.(New) The method of claim 55 wherein step (b) comprises gel electrophoresis.

59.(New) The method of claim 55 wherein the database of migration values comprises migration values of alleles of a gene selected from the group consisting of HLA, TAP, LMP, ras, non-classical HLA and Bf.

60.(New) The method of claim 59 wherein the database of migration values comprises migration values for HLA alleles.

61.(New) The method of claim 60 wherein the HLA alleles are selected from the group consisting of mammalian HLA alleles and human HLA alleles.

62.(New) The method of claim 60 wherein the DNA molecule comprises a portion of an HLA gene.

63.(New) The method of claim 55 further comprising confirming the identity of the DNA molecule by sequencing the test duplex, performing sequence specific primer amplification analysis on the test duplex or performing sequence specific oligonucleotide analysis on the test duplex.

64.(New) The method of claim 55 wherein the method can resolve a difference of one, two or three nucleic acid positions between the DNA molecule and the complementary sequence of the complementary reference DNA strand.

65.(New) The method of claim 55 wherein the DNA molecule and complementary reference DNA strand have the same number of nucleotides.

66.(New) The method of claim 55 wherein the complementary reference DNA strand consists of the wild type sequence of a naturally occurring DNA strand of interest or a naturally occurring mutant thereof.

67.(New) The method of claim 55 wherein the at least one control duplex comprises (i) duplexes which have faster and slower mobility than the test duplex or (ii) duplexes which have graded mobilities.

68.(New) The method of claim 55 wherein the identified DNA molecule is matched to a second identified DNA molecule and the method is used to match tissue between a prospective tissue donor and a prospective tissue recipient.

69.(New) The method of claim 55 further comprising amplifying the DNA molecule prior to step (a).

70.(New) A kit for identifying a DNA molecule, comprising instructions for carrying out the method of claim 1.

71.(New) The kit of claim 70 further comprising one or more of:

- (i) at least one labeled control duplex;
- (ii) control duplexes which have faster and slower mobility than the test duplex;
- (iii) duplexes which have graded mobilities;
- (iv) a primer for amplifying the DNA molecule; and
- (v) a database of migration values of identified DNA molecules.

72.(New) A computer system including a database, the database of values comprising the values set forth in any of table 2, table 3, FIG. 9, FIG. 10, FIG. 11, FIG. 12, FIG. 13, or FIG. 14, wherein the data is used to identify a portion of an HLA gene.

73.(New) A method for identifying a DNA molecule, comprising:

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- (a) amplifying a DNA molecule to produce amplified double stranded DNA molecules;
 - (b) denaturing the amplified double stranded DNA molecules into stranded DNA molecules wherein the single stranded DNA molecules include sense and antisense strands;
 - (c) hybridizing the single stranded DNA molecules with reference DNA strands which are complementary to the single stranded DNA molecules to form test duplexes;
 - (d) separating the test duplexes from at least one control duplex run in the same separation;
 - (e) detecting the positions to which the test duplexes and the at least one control duplex migrate in the separation;
 - (f) assigning an exact migration value to the position to which the test duplex migrates; and
 - (g) identifying the DNA molecule by matching the exact migration with a database of migration values of identified DNA molecules.

74.(New) The method of claim 73 wherein the reference DNA strands are labeled.

75.(New) The method of claim 73 further comprising repeating steps (a)—(g) one or more times wherein a different complementary reference strand is utilized in each repeat of steps (a)—(g) to identify the DNA molecule.

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76.(New) The method of claim 73 wherein step (f) comprises:

- (i) assigning a migration value to the at least one control duplex; and
- (ii) assigning the exact migration value to the test duplex based on the relative migration position of the test duplex compared to the migration value of the control duplex.

REMARKS

After entry of this amendment, Claims 55-76 are pending in the application, Claims 39-54 have been canceled. The present amendment adds no new matter and is otherwise proper. Entry of the amendment in its entirety is respectfully requested. Support for these claims is found throughout the application as filed, including, but not limited to: